Remarks

Claims 13, 15 and 16 are pending in the application. Claims 1, 2, 5-12, 17 and 18 have been cancelled without prejudice to the filing of one or more divisional applications. The description of the claimed antibody as an isolated human monoclonal rabies virus-neutralizing antibody from original claim 3 has been inserted into claim 13. The same characterization has been inserted into the antibody claim 16. Claim 14 has been cancelled as redundant in view of the amendment to claim 13. The dependency of claim 15 has been shifted from claim 14 to claim 13.

Claims 13, 15 and 16 have been rejected as allegedly defining non-statutory subject matter. Claims 13 and 16 have been amended to insert the feature that the antibody is "isolated", as suggested by Examiner.

Claims 13 and 15 have been rejected as containing subject matter allegedly not supported by the written description of Section 112. The rejection alleges that the recitations of sequence homology in claims 13 and 15 are not supported by the disclosure, and constitutes new matter. Claims 13 and 15 have been further rejected as indefinite. The rejection maintains that "homology" or sequence similarity can be calculated by different methods, and that the term "homology" refers to evolutionary origin, not sequence similarity.

Claims 13 and 15 have been amended to substitute the term "identity" for "homology". It is respectfully submitted that the specification at page 12, line 16-20, communicates the meaning of sequence *identity*, not evolutionary homology. Thus, the amendment is supported by the specification.

The specification recites at page 12, lines 5-6 that the invention is directed not only to the specific antibodies described in the specification, but also to "functional equivalents" thereof. At line 13, such "functional equivalents" are stated to include polypeptides with amino acid sequences "substantially the same" as the amino acid sequences of the variable or hypervariable regions of the antibodies of the invention. A sequence that is "substantially the same" as another is defined at lines 16-18 as "a sequence with at least 70%, preferably at least about 80%, and more preferably at least about 90%, sequence homology with another amino acid sequence". Thus, it is respectfully submitted that the claim limitations of "at least 80% amino acid sequence

identity" and "at least 90% amino acid sequence identity" with respect to sequence similarity to SEQ ID NOS:3 and 4 is supported by the specification.

Furthermore, the definition of "substantially the same" in the specification points out that "homology", i.e. sequence identity, is to be determined by the well-known FASTA search method of Pearson and Lipman. *Proc. Natl. Acad. Sci* USA 85:2444-2448 (1988). See page 12, lines 19-20. It is respectfully submitted that the claimed sequence identity percentages are not indefinite, as the specification provides that sequence identity between amino acid sequences is to be determined by the FASTA method.

Conclusion

Based on the foregoing, 13, 15 and 16 are believed to be in condition for allowance. An early and favorable action toward that end is earnestly solicited.

Respectfully submitted,

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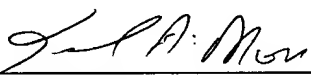
By 

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